In the Specification

Please substitute the following paragraph on page 14, line 26:

Methods for comparing the identity and homology of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J *et al*, 1984), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % homology between two polypeptide sequences. BESTFIT uses the "local homology" algorithm of Smith and Waterman (1981) and finds the best single region of similarity between two sequences. Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F *et al*, 1990, Altschul S F *et al*, 1997, accessible through the home page of the NCBI at ~~www~~See Worldwide Website.ncbi.nlm.nih.gov) and FASTA (Pearson W R, 1990; Pearson 1988).

Please substitute the following paragraph on page 18, beginning at line 11:

INSP035 may thus be fused to another protein, polypeptide or the like, e.g., an immunoglobulin or a fragment thereof. The fusion may be direct, or via a short linker peptide which can be as short as 1 to 3 amino acid residues in length or longer, for example, 13 amino acid residues in length. Said linker may be a tripeptide of the sequence E-F-M (Glu-Phe-Met), for example, or a 13-amino acid linker sequence comprising Glu-Phe-Gly-Ala-Gly-Leu-Val-Leu-Gly-Gly-Gln-Phe-Met (SEQ ID NO:12) introduced between the INSP035 sequence and the immunoglobulin sequence.

Please substitute the following Table 4 on page 30:

Table 4. Sequencing and mutagenesis primers

Primer	**Sequence (5'-3')**
INSP035-MF	ACA AAA AAG CAG GCT TCG AAG GAG ATG CCA CCA TGT CCC TGG G (SEQ ID NO:13)
INSP035-MR	CCC CAG GGA CAT GGT GGC ATC TCC TTC GAA GCC TGC TTT TTT G (SEQ ID NO:14)
21M13	TGT AAA ACG ACG GCC AGT (SEQ ID NO:15)
M13REV	CAG GAA ACA GCT ATG ACC (SEQ ID NO:16)
T7 primer	TAA TAC GAC TCA CTA TAG GG (SEQ ID NO:17)
pDEST14-R	TGG CAG CAG CCA ACT CAG CTT (SEQ ID NO:18)

Please substitute the following paragraph on page 30, beginning at line 19:

PCR primers for human INSP035 and the housekeeping control gene glyceraldehyde 3-phosphate dehydrogenase (GAPDH) were designed using the Primer Express software (PE Biosystems). The primers selected were h-INSP035-169F1 (AGGGCCCAAGCCAAACC) (SEQ ID NO:19) and h-INSP035-281R1 (TCCTGCGCCTGCATCTCC) (SEQ ID NO:20). The specificity and the optimal primer concentration to use for the TaqMan analysis were determined by testing the INSP035 gene-specific primers on a series of dilutions of plasmid pCR-XL-TOPO-INSP035. Potential genomic DNA contamination of the cDNA was excluded by performing PCR reactions using primers specific for GAPDH intronic sequence. The absence of non-specific amplification was controlled by analyzing the PCR products on 4% agarose gels to ensure a single band of the expected molecular weight was produced.

Please replace pages 1-6 (Sequence Listing) with new pages 1-8 attached hereto.